

# CLASSIFICATION: HEAVY CONSTANT CHAINS (cont'd)

- 97) MOPC173: MOUSE IGG2A
- 98) CBPC101: MOUSE IGG2A
- 99) IGA'CL: MOUSE IGA
- 100) IGA'CL: MOUSE IGA
- 101) MOPC47A: MOUSE IGA
- 102) MOPC315: MOUSE IGA
- 103) MOPC311: MOUSE IGA
- 104) IGE'CL: MOUSE IGE
- 105) IGE'CL: MOUSE IGE
- 106) IGE a'CL: MOUSE IGE
- 107) IGE b'CL: MOUSE IGE
- 108) IGE M2B'CL: MOUSE IGE MEMBRANE BOUND
- 109) IR-731: RAT IGD
- 110) IR-731c'CL: RAT IGG2c
- 111) RAT IGG2a'CL: RAT IGG2a
- 112) RAT IGG2b'CL: RAT IGG2b
- 113) RAT IGG1'CL: RAT IGG1
- 114) RAT IGG2b'CL: RAT IGG2b
- 115) IR2'CL: RAT IGE
- 116) PK3'CL: RABBIT MU CHAIN SECRETED (ALLOTYPE A2)
- 117) RABBIT IGG: RABBIT IGG
- 118) PCAN001-12.14'CL: RABBIT IGG
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## GENERAL NOTES: HEAVY CONSTANT CHAINS

# CH1, HINGE, CH2, CH3 AND CH4 DOMAINS ARE TABULATED TO CONFORM TO THEIR CODING NUCLEOTIDE SEQUENCES RELATIVE TO INTERVENING SEQUENCES ESTABLISHED BY SAKANO, H., ROGER, J.H., HUPPI, K., BRACK, C., TRAUNECKER, A., MAKI, R., WALL, R. & TONEGAWA, S. (1979) NATURE, 277, 627-633. A MEMBRANE DOMAIN IS LISTED SEPARATELY TO INCLUDE PART OF THE C-TERMINAL PORTION OF MEMBRANE BOUND IMMUNOGLOBULINS. IF IT IS DESIRED TO ALIGN THE LIGHT CHAIN WITH THE HEAVY CHAIN DOMAINS FOR HOMOLOGY, THE SEQUENTIAL NUMBERING IN THE FIRST COLUMN SHOULD BE USED: RESIDUES 108 TO 215 FOR CL; 114 TO 223 IN CH1 PLUS THE FIRST PART OF HINGE (224 TO 241), THE END OF HINGE (242 AND 243) AND THE FIRST TWO RESIDUES OF CH2 (244 AND 245); 246 THROUGH 361 OF CH2; 362 THROUGH 496 OF CH3; AND 497 THROUGH 628 OF CH4. GAPS IN THE SEQUENTIAL NUMBERING ARE USED FOR ALIGNMENT.

# DISULFIDE BONDS ARE LOCATED AT THE FOLLOWING POSITIONS IF CYS IS PRESENT:

|                |   |
|----------------|---|
| INTRACHAIN:    | 142-208, 274-340, 249-312, 390-456, 524-587.  |
| HL-INTERCHAIN: | 127 OR 128, 198 OR 225, 230, 235.   |
| HH-INTERCHAIN: | 232, 233, 237, 238, 239, 240, 241A, G, M, P, V, BB, EE, KK, QQ, 242, 248, 261, 314. |
| INTERSUBUNIT:  | 328, 444.   |
| TO J-CHAIN:    | 495, 627.   |

IDENTIFICATIONS OF SOME OF THESE DISULFIDE BONDS ARE NOT ABSOLUTELY CERTAIN.

# THERE WOULD APPEAR TO BE POLYMORPHISM AMONG GAL, OU, SCO AND BOT/CO MU-CHAINS AS FOLLOWS:

|     |                  |
|-----|------------------|
| GAL | SER-334, VAL-358 |
|-----|------------------|

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**SPECIFIC NOTES: HEAVY CONSTANT CHAINS**

[illegible]

**SPECIFIC NOTES: HEAVY CONS**

143) SHEEP pSEC'CL: TRANSLATED  
144) HORSE IGG: AS COMPARED WI  
147) CHICKEN IGM'CL: THE AMINO  
148) Elops VE'CL: FROM Elops sa  
152) *Xenopus laevis* c8(II)'CL:  
153) *Xenopus laevis* c14(II)'CL:

- THE FOLLOWING WERE EQUALLY A

| AT POSITION |      |
|-------------|------|
| 113D        |      |
| 113E        | (ILE |
| 127         |      |
| 127B        |      |
| 2274        |      |
| 2241B       |      |
| 2251I       |      |
| 307         |      |
| 3077        |      |
| 336         |      |
| 3362        |      |
| 3363        |      |
| 4033        | A    |
| 4032        |      |
| 4036C       |      |
| 5031        |      |
| 5032        |      |
| 5033        |      |
| 6030B       |      |
| 6037        |      |
| 6037        |      |
| 6038        |      |
| 6039        |      |

**SPECIFIC NOTES: HEAVY CONSTANT CHAINS** (cont'd)

- 143) **SHEEP pSHC'CL**: TRANSLATED FROM cDNA OF SHEEP LYMPHOCYTES  
 144) **HORSE IGG**: AS COMPARED WITH HORSE IGG, THE HORSE T PROTEIN HAD VAL AT POSITION 463, GLU AT 464, AND HIS AT 474.  
 147) **CHICKEN IGM'CL**: THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE SEQUENCE OF A CLONE OF CHICKEN CDNA.  
 148) **Elops VH'CL**: FROM Elops saurus (LADYFISH).  
 152) **Xenopus laevis c8(II)'CL**: ALSO KNOWN AS XIg8'CL.  
 153) **Xenopus laevis c14(II)'CL**: ALSO KNOWN AS XIg14'CL.

+ THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

| AT POSITION | RESIDUES               |
|-------------|------------------------|
| 113D        | (ILE, GLN), (ILE, GLU) |
| 113E        | (CYS, SER)             |
| 137         | (THR, SER)             |
| 158         | (LYS, ASN)             |
| 224         | (ARG, GLU)             |
| 241B        | (PRO, CYS)             |
| 243I        | (ALA, SER)             |
| 281         | (PRO, GLU)             |
| 307         | (PRO, LYS)             |
| 326         | (PRO, THR)             |
| 343         | (THR, ASN)             |
| 351A        | (LEU, THR, ASN)        |
| 403         | (THR, ASN)             |
| 452         | (ASP, ASN)             |
| 496C        | (PRO, ALA)             |
| 511         | (ARG, GLU)             |
| 532         | (ALA, GLU)             |
| 545         | (PRO, LEU)             |
| 580B        | (MET, ASP)             |
| 637         | (LEU, VAL)             |
| 657         | (GLU, GLN)             |
| 662         | (ILE, VAL, ALA)        |
| 663         | (ILE, SER)             |

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